

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Murgita, Robert A.
- (ii) TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS A  
CELL PROLIFERATIVE AGENT
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Fish & Richardson P.C.  
(B) STREET: 225 Franklin Street, Suite 3100  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/377,316  
(B) FILING DATE: 24-JAN-1995  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Clark, Paul T.  
(B) REGISTRATION NUMBER: 30,162  
(C) REFERENCE/DOCKET NUMBER: 06727/006001
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (617) 542-5070  
(B) TELEFAX: (617) 542-8906  
(C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2022 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATATTGTGCT TCCACCACTG CCAATAACAA AATAACTAGC AACCATGAAG TGGGTGGAAT 60  
CAATTTTTTT AATTTTCCTA CTAAATTTTA CTGAATCCAG AACACTGCAT AGAAATGAAT 120  
ATGGAATAGC TTCCATATTG GATTCTTACC AATGTACTGC AGAGATAAGT TTAGCTGACC 180  
TGGCTACCAT ATTTTTTGCC CAGTTTGTTT AAGAAGCCAC TTACAAGGAA GTAAGCAAAA 240

TGGTGAAAGA TGCATTGACT GCAATTGAGA AACCCACTGG AGATGAACAG TCTTCAGGGT 300  
 GTTTAGAAAA CCAGCTACCT GCCTTTCTGG AAGAACTTTG CCATGAGAAA GAAATTTTGG 360  
 AGAAGTACGG ACATTTCAGAC TGCTGCAGCC AAAGTGAAGA GGAAGACAT AACTGTTTTT 420  
 TTGCACACAA AAAGCCCACT GCAGCATGGA TCCCACTTTT CCAAGTTCCA GAACCTGTCA 480  
 CAAGCTGTGA AGCATATGAA GAAGACAGGG AGACATTCAT GAACAAATTC ATTTATGAGA 540  
 TAGCAAGAAG GCATCCCTTC CTGTATGCAC CTACAATTCT TCTTTCGGCT GCTGGGTATG 600  
 AGAAAATAAT TCCATCTTGC TGCAAAGCTG AAAATGCAGT TGAATGCTTC CAAACAAAGG 660  
 CAGCAACAGT TACAAAAGAA TTAAGAGAAA GCAGCTTGTT AAATCAACAT GCATGTCCAG 720  
 TAATGAAAAA TTTTGGGACC CGAACTTTCC AAGCCATAAC TGTTACTAAA CTGAGTCAGA 780  
 AGTTTACCAA AGTTAATTTT ACTGAAATCC AGAACTAGT CCTGGATGTG GCCCATGTAC 840  
 ATGAGCACTG TTGCAGAGCA GATGTGCTGG ATTGTCTGCA GGATGGGGAA AAAATCATGT 900  
 CCTACATATG TTCTCAACAA GACACTCTGT CAAACAAAT AACAGAATGC TGCAAACCTGA 960  
 CCACGCTGGA ACGTGGTCAA TGTATAATTC ATGCAGAAAA TGATGAAAAA CCTGAAGGTC 1020  
 TATCTCCAAA TCTAAACAGG TTTTTAGGAG ATAGAGATTT TAACCAATTT TCTTCAGGGG 1080  
 AAAAAAATAT CTTCTTGCCA AGTTTTGTTC ATGAATATTC AAGAAGACAT CCTCAGCTTG 1140  
 CTGTCTCAGT AATTCTAAGA GTTGCTAAAG GATACCAGGA GTTATTGGAG AAGTGTTCCT 1200  
 AGACTGAAAA CCCTCTTGAA TGCCAAGATA AAGGAGAAGA AGAATTACAG AAATACATCC 1260  
 AGGAGAGCCA AGCATTGGCA AAGCGAAGCT GCGGCCTCTT CCAGAAACTA GGAGAATATT 1320  
 ACTTACAAAA TGAGTTTCTC GTTGCTTACA CAAAGAAAGC CCCCAGCTG ACCTCGTCGG 1380  
 AGCTGATGGC CATCACCAGA AAAATGGCAG CCACAGCAGC CACTTGTTGC CAACTCAGTG 1440  
 AGGACAAACT ATTGGCCTGT GCGGAGGGAG CGGCTGACAT TATTATCGGA CACTTATGTA 1500  
 TCAGACATGA AATGACTCCA GTAAACCCTG GTGTTGGCCA GTGCTGCACT TCTTCATATG 1560  
 CCAACAGGAG GCCATGCTTC AGCAGCTTGG TGGTGGATGA AACATATGTC CCTCCTGCAT 1620  
 TCTCTGATGA CAAGTTCATT TTCCATAAGG ATCTGTGCCA AGCTCAGGGT GTAGCGCTGC 1680  
 AAAGGATGAA GCAAGAGTTT CTCATTAACC TTGTGAAGCA AAAGCCACAA ATAACAGAGG 1740  
 AACAACTTGA GGCTCTCATT GCAGATTTCT CAGGCCTGTT GGAGAAATGC TGCCAAGGCC 1800  
 AGGAACAGGA AGTCTGCTTT GCTGAAGAGG GACAAAAACT GATTTCAAAA ACTGGTGCTG 1860  
 CTTTGGGAGT TTAAATTACT TCAGGGGAAG AGAAGACAAA ACGAGTCTTT CATTCGGTGT 1920  
 GAACTTTTCT CTTTAATTTT AACTGATTTA ACACTTTTTG TGAATTAATG ATAAAGACTT 1980  
 TTATGTGAGA TTTCTTATC ACAGAAATAA AATATCTCCA AA 2022

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 590 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr Leu His Arg Asn Glu Tyr Gly Ile Ala Ser Ile Leu Asp Ser Tyr  
1 5 10 15  
Gln Cys Thr Ala Glu Ile Ser Leu Ala Asp Leu Ala Thr Ile Phe Phe  
20 25 30  
Ala Gln Phe Val Gln Glu Ala Thr Tyr Lys Glu Val Ser Lys Met Val  
35 40 45  
Lys Asp Ala Leu Thr Ala Ile Glu Lys Pro Thr Gly Asp Glu Gln Ser  
50 55 60  
Ser Gly Cys Leu Glu Asn Gln Leu Pro Ala Phe Leu Glu Glu Leu Cys  
65 70 75 80  
His Glu Lys Glu Ile Leu Glu Lys Tyr Gly His Ser Asp Cys Cys Ser  
85 90 95  
Gln Ser Glu Glu Gly Arg His Asn Cys Phe Leu Ala His Lys Lys Pro  
100 105 110  
Thr Ala Ala Trp Ile Pro Leu Phe Gln Val Pro Glu Pro Val Thr Ser  
115 120 125  
Cys Glu Ala Tyr Glu Glu Asp Arg Glu Thr Phe Met Asn Lys Phe Ile  
130 135 140  
Tyr Glu Ile Ala Arg Arg His Pro Phe Leu Tyr Ala Pro Thr Ile Leu  
145 150 155 160  
Leu Ser Ala Ala Gly Tyr Glu Lys Ile Ile Pro Ser Cys Cys Lys Ala  
165 170 175  
Glu Asn Ala Val Glu Cys Phe Gln Thr Lys Ala Ala Thr Val Thr Lys  
180 185 190  
Glu Leu Arg Glu Ser Ser Leu Leu Asn Gln His Ala Cys Pro Val Met  
195 200 205  
Lys Asn Phe Gly Thr Arg Thr Phe Gln Ala Ile Thr Val Thr Lys Leu  
210 215 220  
Ser Gln Lys Phe Thr Lys Val Asn Phe Thr Glu Ile Gln Lys Leu Val  
225 230 235 240  
Leu Asp Val Ala His Val His Glu His Cys Cys Arg Ala Asp Val Leu  
245 250 255  
Asp Cys Leu Gln Asp Gly Glu Lys Ile Met Ser Tyr Ile Cys Ser Gln  
260 265 270  
Gln Asp Thr Leu Ser Asn Lys Ile Thr Glu Cys Cys Lys Leu Thr Thr  
275 280 285

Leu Glu Arg Gly Gln Cys Ile Ile His Ala Glu Asn Asp Glu Lys Pro  
 290 295 300  
 Glu Gly Leu Ser Pro Asn Leu Asn Arg Phe Leu Gly Asp Arg Asp Phe  
 305 310 315 320  
 Asn Gln Phe Ser Ser Gly Glu Lys Asn Ile Phe Leu Ala Ser Phe Val  
 325 330 335  
 His Glu Tyr Ser Arg Arg His Pro Gln Leu Ala Val Ser Val Ile Leu  
 340 345 350  
 Arg Val Ala Lys Gly Tyr Gln Glu Leu Leu Glu Lys Cys Phe Gln Thr  
 355 360 365  
 Glu Asn Pro Leu Glu Cys Gln Asp Lys Gly Glu Glu Glu Leu Gln Lys  
 370 375 380  
 Tyr Ile Gln Glu Ser Gln Ala Leu Ala Lys Arg Ser Cys Gly Leu Phe  
 385 390 395 400  
 Gln Lys Leu Gly Glu Tyr Tyr Leu Gln Asn Glu Phe Leu Val Ala Tyr  
 405 410 415  
 Thr Lys Lys Ala Pro Gln Leu Thr Ser Ser Glu Leu Met Ala Ile Thr  
 420 425 430  
 Arg Lys Met Ala Ala Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu Asp  
 435 440 445  
 Lys Leu Leu Ala Cys Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly His  
 450 455 460  
 Leu Cys Ile Arg His Glu Met Thr Pro Val Asn Pro Gly Val Gly Gln  
 465 470 475 480  
 Cys Cys Thr Ser Ser Tyr Ala Asn Arg Arg Pro Cys Phe Ser Ser Leu  
 485 490 495  
 Val Val Asp Glu Thr Tyr Val Pro Pro Ala Phe Ser Asp Asp Lys Phe  
 500 505 510  
 Ile Phe His Lys Asp Leu Cys Gln Ala Gln Gly Val Ala Leu Gln Arg  
 515 520 525  
 Met Lys Gln Glu Phe Leu Ile Asn Leu Val Lys Gln Lys Pro Gln Ile  
 530 535 540  
 Thr Glu Glu Gln Leu Glu Ala Leu Ile Ala Asp Phe Ser Gly Leu Leu  
 545 550 555 560  
 Glu Lys Cys Cys Gln Gly Gln Glu Gln Glu Val Cys Phe Ala Glu Glu  
 565 570 575  
 Gly Gln Lys Leu Ile Ser Lys Thr Gly Ala Ala Leu Gly Val  
 580 585 590

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Leu His Arg Asn Glu Tyr Gly Ile Ala Ser Ile Leu Asp Ser Tyr  
1 5 10 15  
Gln Cys Thr Ala Glu Ile Ser Leu Ala Asp Leu Ala Thr Ile Phe Phe  
20 25 30  
Ala Gln Phe Val Gln Glu Ala Thr Tyr Lys Glu Val Ser Lys Met Val  
35 40 45  
Lys Asp Ala Leu Thr Ala Ile Glu Lys Pro Thr Gly Asp Glu Gln Ser  
50 55 60  
Ser Gly Cys Leu Glu Asn Gln Leu Pro Ala Phe Leu Glu Glu Leu Cys  
65 70 75 80  
His Glu Lys Glu Ile Leu Glu Lys Tyr Gly His Ser Asp Cys Cys Ser  
85 90 95  
Gln Ser Glu Glu Gly Arg His Asn Cys Phe Leu Ala His Lys Lys Pro  
100 105 110  
Thr Ala Ala Trp Ile Pro Leu Phe Gln Val Pro Glu Pro Val Thr Ser  
115 120 125  
Cys Glu Ala Tyr Glu Glu Asp Arg Glu Thr Phe Met Asn Lys Phe Ile  
130 135 140  
Tyr Glu Ile Ala Arg Arg His Pro Phe Leu Tyr Ala Pro Thr Ile Leu  
145 150 155 160  
Leu Ser Ala Ala Gly Tyr Glu Lys Ile Ile Pro Ser Cys Cys Lys Ala  
165 170 175  
Glu Asn Ala Val Glu Cys Phe Gln Thr Lys Ala Ala Thr Val Thr Lys  
180 185 190  
Glu Leu Arg Glu Ser  
195

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Leu Leu Asn Gln His Ala Cys Pro Val Met Lys Asn Phe Gly Thr  
1 5 10 15

Arg Thr Phe Gln Ala Ile Thr Val Thr Lys Leu Ser Gln Lys Phe Thr  
 20 25 30  
 Lys Val Asn Phe Thr Glu Ile Gln Lys Leu Val Leu Asp Val Ala His  
 35 40 45  
 Val His Glu His Cys Cys Arg Ala Asp Val Leu Asp Cys Leu Gln Asp  
 50 55 60  
 Gly Glu Lys Ile Met Ser Tyr Ile Cys Ser Gln Gln Asp Thr Leu Ser  
 65 70 75 80  
 Asn Lys Ile Thr Glu Cys Cys Lys Leu Thr Thr Leu Glu Arg Gly Gln  
 85 90 95  
 Cys Ile Ile His Ala Glu Asn Asp Glu Lys Pro Glu Gly Leu Ser Pro  
 100 105 110  
 Asn Leu Asn Arg Phe Leu Gly Asp Arg Asp Phe Asn Gln Phe Ser Ser  
 115 120 125  
 Gly Glu Lys Asn Ile Phe Leu Ala Ser Phe Val His Glu Tyr Ser Arg  
 130 135 140  
 Arg His Pro Gln Leu Ala Val Ser Val Ile Leu Arg Val Ala Lys Gly  
 145 150 155 160  
 Tyr Gln Glu Leu Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu  
 165 170 175  
 Cys Gln Asp Lys Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser  
 180 185 190

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln Ala Leu Ala Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu  
 1 5 10 15  
 Tyr Tyr Leu Gln Asn Glu Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro  
 20 25 30  
 Gln Leu Thr Ser Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala  
 35 40 45  
 Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys  
 50 55 60  
 Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His  
 65 70 75 80



130 135 140

Tyr Glu Ile Ala Arg Arg His Pro Phe Leu Tyr Ala Pro Thr Ile Leu  
 145 150 155 160

Leu Ser Ala Ala Gly Tyr Glu Lys Ile Ile Pro Ser Cys Cys Lys Ala  
 165 170 175

Glu Asn Ala Val Glu Cys Phe Gln Thr Lys Ala Ala Thr Val Thr Lys  
 180 185 190

Glu Leu Arg Glu Ser Ser Leu Leu Asn Gln His Ala Cys Pro Val Met  
 195 200 205

Lys Asn Phe Gly Thr Arg Thr Phe Gln Ala Ile Thr Val Thr Lys Leu  
 210 215 220

Ser Gln Lys Phe Thr Lys Val Asn Phe Thr Glu Ile Gln Lys Leu Val  
 225 230 235 240

Leu Asp Val Ala His Val His Glu His Cys Cys Arg Ala Asp Val Leu  
 245 250 255

Asp Cys Leu Gln Asp Gly Glu Lys Ile Met Ser Tyr Ile Cys Ser Gln  
 260 265 270

Gln Asp Thr Leu Ser Asn Lys Ile Thr Glu Cys Cys Lys Leu Thr Thr  
 275 280 285

Leu Glu Arg Gly Gln Cys Ile Ile His Ala Glu Asn Asp Glu Lys Pro  
 290 295 300

Glu Gly Leu Ser Pro Asn Leu Asn Arg Phe Leu Gly Asp Arg Asp Phe  
 305 310 315 320

Asn Gln Phe Ser Ser Gly Glu Lys Asn Ile Phe Leu Ala Ser Phe Val  
 325 330 335

His Glu Tyr Ser Arg Arg His Pro Gln Leu Ala Val Ser Val Ile Leu  
 340 345 350

Arg Val Ala Lys Gly Tyr Gln Glu Leu Leu Glu Lys Cys Phe Gln Thr  
 355 360 365

Glu Asn Pro Leu Glu Cys Gln Asp Lys Gly Glu Glu Glu Leu Gln Lys  
 370 375 380

Tyr Ile Gln Glu Ser  
 385

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:



Ser Leu Leu Asn Gln His Ala Cys Pro Val Met Lys Asn Phe Gly Thr  
 1 5 10 15  
 Arg Thr Phe Gln Ala Ile Thr Val Thr Lys Leu Ser Gln Lys Phe Thr  
 20 25 30  
 Lys Val Asn Phe Thr Glu Ile Gln Lys Leu Val Leu Asp Val Ala His  
 35 40 45  
 Val His Glu His Cys Cys Arg Ala Asp Val Leu Asp Cys Leu Gln Asp  
 50 55 60  
 Gly Glu Lys Ile Met Ser Tyr Ile Cys Ser Gln Gln Asp Thr Leu Ser  
 65 70 75 80  
 Asn Lys Ile Thr Glu Cys Cys Lys Leu Thr Thr Leu Glu Arg Gly Gln  
 85 90 95  
 Cys Ile Ile His Ala Glu Asn Asp Glu Lys Pro Glu Gly Leu Ser Pro  
 100 105 110  
 Asn Leu Asn Arg Phe Leu Gly Asp Arg Asp Phe Asn Gln Phe Ser Ser  
 115 120 125  
 Gly Glu Lys Asn Ile Phe Leu Ala Ser Phe Val His Glu Tyr Ser Arg  
 130 135 140  
 Arg His Pro Gln Leu Ala Val Ser Val Ile Leu Arg Val Ala Lys Gly  
 145 150 155 160  
 Tyr Gln Glu Leu Leu Glu Lys Cys Phe Gln Thr Glu Asn Pro Leu Glu  
 165 170 175  
 Cys Gln Asp Lys Gly Glu Glu Glu Leu Gln Lys Tyr Ile Gln Glu Ser  
 180 185 190  
 Gln Ala Leu Ala Lys Arg Ser Cys Gly Leu Phe Gln Lys Leu Gly Glu  
 195 200 205  
 Tyr Tyr Leu Gln Asn Glu Phe Leu Val Ala Tyr Thr Lys Lys Ala Pro  
 210 215 220  
 Gln Leu Thr Ser Ser Glu Leu Met Ala Ile Thr Arg Lys Met Ala Ala  
 225 230 235 240  
 Thr Ala Ala Thr Cys Cys Gln Leu Ser Glu Asp Lys Leu Leu Ala Cys  
 245 250 255  
 Gly Glu Gly Ala Ala Asp Ile Ile Ile Gly His Leu Cys Ile Arg His  
 260 265 270  
 Glu Met Thr Pro Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser  
 275 280 285  
 Tyr Ala Asn Arg Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr  
 290 295 300  
 Tyr Val Pro Pro Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp  
 305 310 315 320  
 Leu Cys Gln Ala Gln Gly Val Ala Leu Gln Arg Met Lys Gln Glu Phe  
 325 330 335  
 Leu Ile Asn Leu Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu

|   |     |     |
|---|-----|-----|
| 340   | 345 | 350 |
| Glu Ala Leu Ile Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln |     |     |
| 355   | 360 | 365 |
| Gly Gln Glu Gln Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile |     |     |
| 370   | 375 | 380 |
| Ser Lys Thr Gly Ala Ala Leu Gly Val                             |     |     |
| 385   | 390 |     |

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

*Ala*  
*Control*

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Tyr | Ile | Cys | Ser | Gln | Gln | Asp | Thr | Leu | Ser | Asn | Lys | Ile | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Cys | Cys | Lys | Leu | Thr | Thr | Leu | Glu | Arg | Gly | Gln | Cys | Ile | Ile | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Glu | Asn | Asp | Glu | Lys | Pro | Glu | Gly | Leu | Ser | Pro | Asn | Leu | Asn | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Gly | Asp | Arg | Asp | Phe | Asn | Gln | Phe | Ser | Ser | Gly | Glu | Lys | Asn |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Phe | Leu | Ala | Ser | Phe | Val | His | Glu | Tyr | Ser | Arg | Arg | His | Pro | Gln |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ala | Val | Ser | Val | Ile | Leu | Arg | Val | Ala | Lys | Gly | Tyr | Gln | Glu | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Glu | Lys | Cys | Phe | Gln | Thr | Glu | Asn | Pro | Leu | Glu | Cys | Gln | Asp | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Glu | Glu | Glu | Leu | Gln | Lys | Tyr | Ile | Gln | Glu | Ser | Gln | Ala | Leu | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Arg | Ser | Cys | Gly | Leu | Phe | Gln | Lys | Leu | Gly | Glu | Tyr | Tyr | Leu | Gln |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Glu | Phe | Leu | Val | Ala | Tyr | Thr | Lys | Lys | Ala | Pro | Gln | Leu | Thr | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Glu | Leu | Met | Ala | Ile | Thr | Arg | Lys | Met | Ala | Ala | Thr | Ala | Ala | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Cys | Gln | Leu | Ser | Glu | Asp | Lys | Leu | Leu | Ala | Cys | Gly | Glu | Gly | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Asp | Ile | Ile | Ile | Gly | His | Leu | Cys | Ile | Arg | His | Glu | Met | Thr | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

Val Asn Pro Gly Val Gly Gln Cys Cys Thr Ser Ser Tyr Ala Asn Arg  
 210 215 220

Arg Pro Cys Phe Ser Ser Leu Val Val Asp Glu Thr Tyr Val Pro Pro  
 225 230 235 240

Ala Phe Ser Asp Asp Lys Phe Ile Phe His Lys Asp Leu Cys Gln Ala  
 245 250 255

Gln Gly Val Ala Leu Gln Arg Met Lys Gln Glu Phe Leu Ile Asn Leu  
 260 265 270

Val Lys Gln Lys Pro Gln Ile Thr Glu Glu Gln Leu Glu Ala Leu Ile  
 275 280 285

Ala Asp Phe Ser Gly Leu Leu Glu Lys Cys Cys Gln Gly Gln Glu Gln  
 290 295 300

Glu Val Cys Phe Ala Glu Glu Gly Gln Lys Leu Ile Ser Lys Thr Gly  
 305 310 315 320

Ala Ala Leu Gly Val  
 325

2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAAAAAGGTA CCACACTGCA TAGAAATGAA

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAAAAAGGAT CCTTAGCTTT CTCTTAATTC TTT

33

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAAAAATCG ATATGAGCTT GTTAAATCAA CAT

33

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAAAAAGGAT CCTTAGCTCT CCTGGATGTA TTT

33

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAAAAATCG ATATGCAAGC ATTGGCAAAG CGA

33

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAAAAAGGAT CCTTAACTC CCAAAGCAGC ACG

33

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAAAAAATCG ATATGTCCTA CATATGTTCT CAA

33

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Tyr Ile Cys Ser Gln Gln Asp Thr  
1 5